

Towards an open online repository of *P. polycephalum* networks and their corresponding graph representations*

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The slime mold *Physarum polycephalum* has proven a rich substrate for interdisciplinary research. The study of the structure and function of the organism's signature vein-networks has captured the interest of biologists, physicists and computer scientists in particular.

The generic three-stage research approach consists of *data acquisition*, *data processing* and *data analysis*. Data acquisition includes the preparation and execution of a sufficient number of wet-lab experiments, designed such that large slime mold networks form with high probability. A series of high quality digital images of the growing slime mold constitutes the raw data. Converting the raw data into a series of mathematical graphs has been proposed in [1] as a

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novel data processing step. I.e., for each image of *P. polycephalum* a corresponding weighted planar graph is computed. Subsequently, powerful methods from graph theory and network science can be used to drive data analysis. All three mentioned stages are challenging as they require special resources and expert knowledge. Data acquisition and processing in particular, may quickly become serious obstacles deterring interested researchers from starting to work on *P. polycephalum*.

Our aim is to help remove these obstacles. To this end a large body of raw images documenting the growth of *P. polycephalum* and its networks has been collected at the KIST Europe in repeated experiments. To accurately and efficiently process this data we have introduced a new software tool called NEFI [2] (<http://nefi.mpi-inf.mpg.de/>), allowing users to extract graphs from high quality images using powerful techniques from computer vision and image processing.

Using NEFI we have turned every image of the KIST Europe dataset into a corresponding weighted planar graph. In addition to the topological structure, these graphs encode valuable information such as edge weights and lengths true to the underlying images. Thus we effectively created pairs, (image, graph), which we collect in the publicly available Slime Mold Graph Repository (<http://smgr.mpi-inf.mpg.de/>), allowing researchers instant access to either raw data or the graphs. Furthermore, researchers working on modelling *P. polycephalum* networks may consider testing predictions of their models using the graphs in the repository.

REFERENCES

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